

PCT09

RAW SEQUENCE LISTING

DATE: 09/24/2001

PATENT APPLICATION: US/09/807,345

TIME: 16:35:06

Input Set : A:\ES.txt

Output Set: N:\CRF3\09242001\I807345.raw

3 <110> APPLICANT: ARKHAMMAR, Per O.G. et al.

5 <120> TITLE OF INVENTION: AN IMPROVED METHOD FOR EXTRACTING QUANTITATIVE INFORMATION
RELATING TO AN

6 INFLUENCE IN A CELLULAR RESPONSE

8 <130> FILE REFERENCE: 0459-0571P

10 <140> CURRENT APPLICATION NUMBER: 09/807,345

11 <141> CURRENT FILING DATE: 2001-04-12

13 <160> NUMBER OF SEQ ID NOS: 40

15 <170> SOFTWARE: PatentIn version 3.1

17 <210> SEQ ID NO: 1

18 <211> LENGTH: 1788

19 <212> TYPE: DNA

20 <213> ORGANISM: Aequorea victoria and mouse

22 <220> FEATURE:

23 <221> NAME/KEY: CDS

24 <222> LOCATION: (1)..(1788)

25 <223> OTHER INFORMATION:

28 <400> SEQUENCE: 1

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30 Met Gly Asn Ala Ala Ala Lys Lys Gly Ser Glu Gln Glu Ser Val
31 1 5 10 15
33 aaa gag ttc cta gcc aaa gcc aag gaa gat ttc ctg aaa aaa tgg gaa 96
34 Lys Glu Phe Leu Ala Lys Ala Lys Glu Asp Phe Leu Lys Lys Trp Glu
35 20 25 30
37 gac ccc tct cag aat aca gcc cag ttg gat cag ttt gat aga atc aag 144
38 Asp Pro Ser Gln Asn Thr Ala Gln Leu Asp Gln Phe Asp Arg Ile Lys
39 35 40 45
41 acc ctt ggc acc ggc tcc ttt ggg cga gtg atg ctg gtg aag cac aag 192
42 Thr Leu Gly Thr Gly Ser Phe Gly Arg Val Met Leu Val Lys His Lys
43 50 55 60
45 gag agt ggg aac cac tac gcc atg aag atc tta gac aag cag aag gtg 240
46 Glu Ser Gly Asn His Tyr Ala Met Lys Ile Leu Asp Lys Gln Lys Val
47 65 70 75 80
49 gtg aag cta aag cag atc gag cac act ctg aat gag aag cgc atc ctg 288
50 Val Lys Leu Lys Gln Ile Glu His Thr Leu Asn Glu Lys Arg Ile Leu
51 85 90 95
53 cag gcc gtc aac ttc ccg ttc ctg gtc aaa ctt gaa ttc tcc ttc aag 336
54 Gln Ala Val Asn Phe Pro Phe Leu Val Lys Leu Glu Phe Ser Phe Lys
55 100 105 110
57 gac aac tca aac ctg tac atg gtc atg gag tat gta gct ggt ggc gag 384
58 Asp Asn Ser Asn Leu Tyr Met Val Met Glu Tyr Val Ala Gly Gly Glu
59 115 120 125
61 atg ttc tcc cac cta cgg cgg att gga agg ttc agc gag ccc cat gcc 432
62 Met Phe Ser His Leu Arg Arg Ile Gly Arg Phe Ser Glu Pro His Ala
63 130 135 140
65 cgt ttc tac gcg gcg cag atc gtc ctg acc ttt gag tat ctg cac tcc 480
66 Arg Phe Tyr Ala Ala Gln Ile Val Leu Thr Phe Glu Tyr Leu His Ser
67 145 150 155 160

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69 ctg gac ctc atc tac cgg gac ctg aag ccc gag aat ctt ctc atc gac      528
70 Leu Asp Leu Ile Tyr Arg Asp Leu Lys Pro Glu Asn Leu Leu Ile Asp
71      165      170      175
73 cag cag ggc tat att cag gtg aca gac ttc ggt ttt gcc aag cgt gtg      576
74 Gln Gln Gly Tyr Ile Gln Val Thr Asp Phe Gly Phe Ala Lys Arg Val
75      180      185      190
77 aaa ggc cgt act tgg acc ttg tgt ggg acc cct gag tac ttg gcc ccc      624
78 Lys Gly Arg Thr Trp Thr Leu Cys Gly Thr Pro Glu Tyr Leu Ala Pro
79      195      200      205
81 gag att atc ctg agc aaa ggc tac aac aag gct gtg gac tgg tgg gct      672
82 Glu Ile Ile Leu Ser Lys Gly Tyr Asn Lys Ala Val Asp Trp Trp Ala
83      210      215      220
85 ctc gga gtc ctc atc tac gag atg gct gct ggt tac cca ccc ttc ttc      720
86 Leu Gly Val Leu Ile Tyr Glu Met Ala Ala Gly Tyr Pro Pro Phe Phe
87 225      230      235      240
89 gct gac cag cct atc cag atc tat gag aaa atc gtc tct ggg aag gtg      768
90 Ala Asp Gln Pro Ile Gln Ile Tyr Glu Lys Ile Val Ser Gly Lys Val
91      245      250      255
93 cgg ttc cca tcc cac ttc agc tct gac ttg aag gac ctg ctg cgg aac      816
94 Arg Phe Pro Ser His Phe Ser Ser Asp Leu Lys Asp Leu Leu Arg Asn
95      260      265      270
97 ctt ctg caa gtg gat cta acc aag cgc ttt gga aac ctc aag gac ggg      864
98 Leu Leu Gln Val Asp Leu Thr Lys Arg Phe Gly Asn Leu Lys Asp Gly
99      275      280      285
101 gtc aat gac atc aag aac cac aag tgg ttt gcc acg act gac tgg att      912
102 Val Asn Asp Ile Lys Asn His Lys Trp Phe Ala Thr Thr Asp Trp Ile
103      290      295      300
105 gcc atc tat cag aga aag gtg gaa gct ccc ttc ata cca aag ttt aaa      960
106 Ala Ile Tyr Gln Arg Lys Val Glu Ala Pro Phe Ile Pro Lys Phe Lys
107 305      310      315      320
109 ggc cct ggg gac acg agt aac ttt gac gac tat gag gag gaa gag atc      1008
110 Gly Pro Gly Asp Thr Ser Asn Phe Asp Asp Tyr Glu Glu Glu Glu Ile
111      325      330      335
113 cgg gtc tcc atc aat gag aag tgt ggc aag gag ttt act gag ttt ggg      1056
114 Arg Val Ser Ile Asn Glu Lys Cys Gly Lys Glu Phe Thr Glu Phe Gly
115      340      345      350
117 cgc gcc atg agt aaa gga gaa gaa ctt ttc act gga gtt gtc cca att      1104
118 Arg Ala Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile
119      355      360      365
121 ctt gtt gaa tta gat ggc gat gtt aat ggg caa aaa ttc tct gtt agt      1152
122 Leu Val Glu Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser Val Ser
123      370      375      380
125 gga gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctt aaa ttt      1200
126 Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe
127 385      390      395      400
129 att tgc act act ggg aag cta cct gtt cca tgg cca acg ctt gtc act      1248
130 Ile Cys Thr Thr Gly Lys Leu Pro Val Trp Pro Thr Leu Val Thr
131      405      410      415
133 act ctc act tat ggt gtt caa tgc ttt tct aga tac cca gat cat atg      1296

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134 Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met
135          420          425          430
137 aaa cag cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag      1344
138 Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln
139          435          440          445
141 gaa aga act ata ttt tac aaa gat gac ggg aac tac aag aca cgt gct      1392
142 Glu Arg Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala
143          450          455          460
145 gaa gtc aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa      1440
146 Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys
147 465          470          475          480
149 ggt att gat ttt aaa gaa gat gga aac att ctt gga cac aaa atg gaa      1488
150 Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu
151          485          490          495
153 tac aat tat aac tca cat aat gta tac atc atg gca gac aaa cca aag      1536
154 Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys
155          500          505          510
157 aat ggc atc aaa gtt aac ttc aaa att aga cac aac att aaa gat gga      1584
158 Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly
159          515          520          525
161 agc gtt caa tta gca gac cat tat caa caa aat act cca att ggc gat      1632
162 Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
163          530          535          540
165 ggc cct gtc ctt tta cca gac aac cat tac ctg tcc acg caa tct gcc      1680
166 Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala
167 545          550          555          560
169 ctt tcc aaa gat ccc aac gaa aag aga gat cac atg atc ctt ctt gag      1728
170 Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Glu
171          565          570          575
173 ttt gta aca gct gct ggg att aca cat ggc atg gat gaa cta tac aaa      1776
174 Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
175          580          585          590
177 cct cag gag taa      1788
178 Pro Gln Glu
179          595
182 <210> SEQ ID NO: 2
183 <211> LENGTH: 595
184 <212> TYPE: PRT
185 <213> ORGANISM: Aequorea victoria and mouse
187 <400> SEQUENCE: 2
189 Met Gly Asn Ala Ala Ala Ala Lys Lys Gly Ser Glu Gln Glu Ser Val
190 1          5          10          15
193 Lys Glu Phe Leu Ala Lys Ala Lys Glu Asp Phe Leu Lys Lys Trp Glu
194          20          25          30
197 Asp Pro Ser Gln Asn Thr Ala Gln Leu Asp Gln Phe Asp Arg Ile Lys
198          35          40          45
201 Thr Leu Gly Thr Gly Ser Phe Gly Arg Val Met Leu Val Lys His Lys
202          50          55          60
205 Glu Ser Gly Asn His Tyr Ala Met Lys Ile Leu Asp Lys Gln Lys Val

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206	65					70						75				80
209	Val	Lys	Leu	Lys	Gln	Ile	Glu	His	Thr	Leu	Asn	Glu	Lys	Arg	Ile	Leu
210					85					90					95	
213	Gln	Ala	Val	Asn	Phe	Pro	Phe	Leu	Val	Lys	Leu	Glu	Phe	Ser	Phe	Lys
214				100					105					110		
217	Asp	Asn	Ser	Asn	Leu	Tyr	Met	Val	Met	Glu	Tyr	Val	Ala	Gly	Gly	Glu
218			115					120					125			
221	Met	Phe	Ser	His	Leu	Arg	Arg	Ile	Gly	Arg	Phe	Ser	Glu	Pro	His	Ala
222		130					135					140				
225	Arg	Phe	Tyr	Ala	Ala	Gln	Ile	Val	Leu	Thr	Phe	Glu	Tyr	Leu	His	Ser
226	145					150					155				160	
229	Leu	Asp	Leu	Ile	Tyr	Arg	Asp	Leu	Lys	Pro	Glu	Asn	Leu	Leu	Ile	Asp
230				165						170					175	
233	Gln	Gln	Gly	Tyr	Ile	Gln	Val	Thr	Asp	Phe	Gly	Phe	Ala	Lys	Arg	Val
234				180					185					190		
237	Lys	Gly	Arg	Thr	Trp	Thr	Leu	Cys	Gly	Thr	Pro	Glu	Tyr	Leu	Ala	Pro
238			195					200					205			
241	Glu	Ile	Ile	Leu	Ser	Lys	Gly	Tyr	Asn	Lys	Ala	Val	Asp	Trp	Trp	Ala
242		210					215					220				
245	Leu	Gly	Val	Leu	Ile	Tyr	Glu	Met	Ala	Ala	Gly	Tyr	Pro	Pro	Phe	Phe
246	225					230					235				240	
249	Ala	Asp	Gln	Pro	Ile	Gln	Ile	Tyr	Glu	Lys	Ile	Val	Ser	Gly	Lys	Val
250				245						250					255	
253	Arg	Phe	Pro	Ser	His	Phe	Ser	Ser	Asp	Leu	Lys	Asp	Leu	Leu	Arg	Asn
254			260						265					270		
257	Leu	Leu	Gln	Val	Asp	Leu	Thr	Lys	Arg	Phe	Gly	Asn	Leu	Lys	Asp	Gly
258			275					280					285			
261	Val	Asn	Asp	Ile	Lys	Asn	His	Lys	Trp	Phe	Ala	Thr	Thr	Asp	Trp	Ile
262		290				295						300				
265	Ala	Ile	Tyr	Gln	Arg	Lys	Val	Glu	Ala	Pro	Phe	Ile	Pro	Lys	Phe	Lys
266	305					310					315				320	
269	Gly	Pro	Gly	Asp	Thr	Ser	Asn	Phe	Asp	Asp	Tyr	Glu	Glu	Glu	Glu	Ile
270				325						330					335	
273	Arg	Val	Ser	Ile	Asn	Glu	Lys	Cys	Gly	Lys	Glu	Phe	Thr	Glu	Phe	Gly
274				340					345					350		
277	Arg	Ala	Met	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile
278			355					360					365			
281	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	Gln	Lys	Phe	Ser	Val	Ser
282		370				375						380				
285	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe
286	385					390					395				400	
289	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr
290				405						410					415	
293	Thr	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met
294				420					425					430		
297	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln
298			435					440					445			
301	Glu	Arg	Thr	Ile	Phe	Tyr	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala
302		450					455					460				

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305 Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys
306 465                               470                               475                               480
309 Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu
310                               485                               490                               495
313 Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys
314                               500                               505                               510
317 Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly
318                               515                               520                               525
321 Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
322                               530                               535                               540
325 Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala
326 545                               550                               555                               560
329 Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Glu
330                               565                               570                               575
333 Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
334                               580                               585                               590
337 Pro Gln Glu
338                               595
341 <210> SEQ ID NO: 3
342 <211> LENGTH: 2751
343 <212> TYPE: DNA
344 <213> ORGANISM: Aequorea victoria and mouse
346 <220> FEATURE:
347 <221> NAME/KEY: CDS
348 <222> LOCATION: (1)..(2751)
349 <223> OTHER INFORMATION:
352 <400> SEQUENCE: 3
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354 Met Ala Asp Val Tyr Pro Ala Asn Asp Ser Thr Ala Ser Gln Asp Val
355 1                               5                               10                               15
357 gcc aac cgc ttc gcc cgc aaa ggg gcg ctg agg cag aag aac gtg cat      96
358 Ala Asn Arg Phe Ala Arg Lys Gly Ala Leu Arg Gln Lys Asn Val His
359                               20                               25                               30
361 gag gtg aaa gac cac aaa ttc atc gcc cgc ttc ttc aag caa ccc acc      144
362 Glu Val Lys Asp His Lys Phe Ile Ala Arg Phe Phe Lys Gln Pro Thr
363                               35                               40                               45
365 ttc tgc agc cac tgc acc gac ttc atc tgg ggg ttt ggg aaa caa ggc      192
366 Phe Cys Ser His Cys Thr Asp Phe Ile Trp Gly Phe Gly Lys Gln Gly
367                               50                               55                               60
369 ttc cag tgc caa gtt tgc tgt ttt gtg gtt cat aag agg tgc cat gag      240
370 Phe Gln Cys Gln Val Cys Cys Phe Val Val His Lys Arg Cys His Glu
371 65                               70                               75                               80
373 ttc gtt acg ttc tct tgt ccg ggt gcg gat aag gga cct gac act gac      288
374 Phe Val Thr Phe Ser Cys Pro Gly Ala Asp Lys Gly Pro Asp Thr Asp
375                               85                               90                               95
377 gac ccc agg agc aag cac aag ttc aaa atc cac aca tac gga agc cct      336
378 Asp Pro Arg Ser Lys His Lys Phe Lys Ile His Thr Tyr Gly Ser Pro
379                               100                              105                              110
381 acc ttc tgt gat cac tgt ggg tcc ctg ctc tat gga ctt atc cac caa      384

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VERIFICATION SUMMARY

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